

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gregory Plowman
Bahija Jallal
- (ii) TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
PTP RELATED DISORDERS
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Lyon & Lyon
(B) STREET: 633 West Fifth Street
Suite 4700
(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 90071-2066
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: FastSEQ for Windows 2.0
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 60/049,756
(B) FILING DATE: June 11, 1997
- (A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Warburg, Richard J.
(B) REGISTRATION NUMBER: 32,327
(C) REFERENCE/DOCKET NUMBER: 235/054

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (213) 489-1600
 (B) TELEFAX: (213) 955-0440
 (C) TELEX: 67-3510

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1785 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGTTATGTCT GACTCACTGC ACTGGAGTTT GGCAAAAGCA TCTCAGAAGT GGTGTGCTT 60
 TTTTGAATGA AATGATCAAT GGAGTGCTCC AGTTGTATGC TGGCCTCTGG ATACTAACTA 120
 GACCTGCCTG ACTCCAGGAA CTAAGGCTCA GTATCTGCAG AAGCTTTTTG CCCATCTCAT 180
 TCCGGCTATG GGGACAACAT GTCTTCACCC AGGAAGGTTA GAGGAAAAAC TGGAAGAGAT 240
 AATGATGAAG AGGAGGGTAA TTCAGGTAAC CTGAATCTCC GCAACTCTTT GCCTTCATCG 300
 AGTCAGAAAA TGACGCCTAC GAAGCCGATT TTTGGGAATA AAATGAATTC AGAGAATGTA 360
 AAACCTCTCC ATCACCTGTC ATTCTCAGAT AAGTATGAGC TTGTTTACCC AGAGCCTTTG 420
 GAAAGTGACA CTGATGAGAC TGTGTGGGAT GTCAGTGACC GGTCTCTCAG AAACAGGTGG 480
 AACAGTATGG ATTCAGAGAC TGCAGGGCCG TCAAAGACTG TCTCCCCAGT GCTTTCTGGT 540
 AGTAGTAGGC TCTCAAAGGA CACTGAAACA TCTGTCTCTG AAAAGGAGCT AACTCAGTTG 600
 GCTCAGATTC GACCATTAAT ATTCAACAGT TCTGCACGGT CTGCTATGCG GGATTGTTTG 660
 AACACGCTTC AGAAAAAAGA AGAAGTTGAT ATCATCCGTG AGTTTTTGGG GTTAGAACAA 720
 ATGACTCTGC CTGATGACTT CAATTCTGGG AATACACTAC AGAACAGAGA TAAGAACAGA 780
 TACCGAGATA TTCTTCCATA TGATTCAACA CGTGTTCCTC TTGGAAAAAA CAAGGACTAC 840
 ATCAACGCTA GTTATATTAG AATAGTAAAT CATGAAGAAG AGTATTTTTA TATTGCCACT 900
 CAAGGACCAT TGCCAGAAAC TATAGAAGAC TTTTGGCAAA TGGTCTCTGA AAATAATTGT 960
 AATGTTATTG CTATGATAAC CAGAGAGATA GAATGTGGAG TTATCAAGTG TTACAGTTAC 1020
 TGGCCCATTT CTCTGAAGGA GCCTTTGGAA TTCGAACACT TTAGTGTCTT TCTGGAGACC 1080
 TTTTCATGTA CCAATATTTT CACCGTTCGA GTATTTTCAGA TTGTGAAGAA GTCCACAGGA 1140
 AAGAGCCAAT GTGTAAACA CTTGCAGTTC ACCAAGTGGC CAGACCATGG CACTCCTGCC 1200
 TCAGCAGATT TTTTCATAAA ATATGTCCGT TATGTGAGGA AGAGCCACAT TACAGGACCC 1260
 CTCCTTGTTT ACTGCAGTGC TGGTGTAGGC CGAACAGGGG TGTTTCATATG TGTGGATGTT 1320
 GTGTTCTCTG CCATCGAGAA GAAGTACTCT TTTGACATTA TGAACATAGT GACCCAGATG 1380
 AGAAAGCAGC GCTGTGGCAT GATTCAAACC AAGGAGCAGT ACCAGTTTGT TTATGAAATT 1440
 GTGCTTGAAG TTCTTCAGAA CCTTCTGGCT TTGTATTAAG AGAGACTTCT GCGCCTGTCC 1500
 CTCGAGGTTA CCGAGCAGCT TGGAGCCTGA GCCGTGCTGA AGCGTCTGCG GGCCGTGCAG 1560
 TCTGCCTTCT GATTTTTCTC TCTGAAAGTC CCTGAAGGTA GCACTACTGG GCACAGAGTG 1620
 AACTGTTTCC ACTTGATCTT TCTGAACAAG AGCAAAATAC CCTCCATGCC TTCTACGGAA 1680
 ACGGAAGTTG CATGAAACAA CCTCCGCTTG GCTGTCTGGT TTGTGGTATT ACAGAGCTTA 1740
 ATAAAAGACT TAGATGTGAA AAAAAAAAAA AAAAAAAAAA AAAAA 1785

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1896 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGTTATGTCT GACTCACTGC ACTGGAGTTT GGCAAAAGCA TCTCAGAAGT GGTGTGCTT 60

TTTTGAATGA	AATGATCAAT	GGAGTGCTCC	AGTTGTATGC	TGGCCTCTGG	ATACTAACTA	120
GACCTGCCTG	ACTCCAGGAA	CTAAGGCTCA	GTATCTGCAG	AAGCTTTTTG	CCCATCTCAT	180
TCCGGCTATG	GGGACAACAT	GTCTTCACCC	AGGAAGGTTA	GAGGAAAAAC	TGGAAGAGAT	240
AATGATGAAG	AGGAGGGTAA	TTCAGGTAAC	CTGAATCTCC	GCAACTCTTT	GCCTTCATCG	300
AGTCAGAAAA	TGACGCCTAC	GAAGCCGGTA	CAAAATAAAA	ATCTCATGAA	GTATGAAGAA	360
CACTTAGATA	TATTGATGGT	GTTTTTATTG	ATAAAAAACCA	TATGGTATAA	TGCTTTCAAA	420
TTATGGAAAG	GCAAGCTTAT	TTTTGGGAAT	AAAATGAATT	CAGAGAATGT	AAAACCCTCC	480
CATCACCTGT	CATTCTCAGA	TAAGTATGAG	CTTGTTTACC	CAGAGCCTTT	GGAAAGTGAC	540
ACTGATGAGA	CTGTGTGGGA	TGTCAGTGAC	CGGTCTCTCA	GAAACAGGTG	GAACAGTATG	600
GATTACAGAG	CTGCAGGGCC	GTCAAAGACT	GTCTCCCCAG	TGCTTCTCTG	TAGTAGTAGG	660
CTCTCAAAGG	ACACTGAAAC	ATCTGTCTCT	GAAAAGGAGC	TAACTCAGTT	GGCTCAGATT	720
CGACCATTAA	TATTCAACAG	TTCTGCACGG	TCTGCTATGC	GGGATTGTTT	GAACACGCTT	780
CAGAAAAAAG	AAGAAGCTGA	TATCATCCGT	GAGTTTTTGG	AGTTAGAACA	AATGACTCTG	840
CCTGATGACT	TCAATTCTGG	GAATACACTA	CAGAACAGAG	ATAAGAACAG	ATACCGAGAT	900
ATTCTTCCAT	ATGATTCAAC	ACGTGTTCTT	CTTGGAAGAA	ACAAGGACTA	CATCAACGCT	960
AGTTATATTA	GAATAGTAAA	TCATGAAGAA	GAGTATTTTT	ATATTGCCAC	TCAAGGACCA	1020
TTGCCAGAAA	CTATAGAAGA	CTTTTGGCAA	ATGGTCTCTG	AAAATAAATTG	TAATGTTATT	1080
GCTATGATAA	CCAGAGAGAT	AGAATGTGGA	GTTATCAAGT	GTTACAGTTA	CTGGCCCAT	1140
TCTCTGAAGG	AGCCTTTTGA	ATTCGAACAC	TTTAGTGTCT	TTCTGGAGAC	CTTTCATGTA	1200
ACTCAATATT	TCACCGTTCG	AGTATTTTCA	ATTGTGAAGA	AGTCCACAGG	AAAGAGCCAA	1260
TGTGTAAAAC	ACTTGCAGTT	CACCAAGTGG	CCAGACCATG	GCACTCCTGC	CTCAGCAGAT	1320
TTTTTCATAA	AATATGTCCG	TTATGTGAGG	AAGAGCCACA	TTACAGGACC	CCTCCTTGTT	1380
CACTGCAGTG	CTGGTGTAGG	CCGAACAGGG	GTGTTTCATAT	GTGTGGATGT	TGTGTTCTCT	1440
GCCATCGAGA	AGAAGTACTC	TTTTGACATT	ATGAACATAG	TGACCCAGAT	GAGAAAGCAG	1500
CGCTGTGGCA	TGATTCAAAC	CAAGGAGCAG	TACCAGTTTT	GTTATGAAAT	TGTGCTTGAA	1560
GTTCTTTTCA	ACCTTCTGGC	TTTGTATTAA	GAGAGACTTC	TGCGCCTGTC	CCTCGAGGTT	1620
ACCGAGCAGC	TTGGAGCCTG	AGCCGTGCTG	AAGCGTCTGC	GGGCCGTGCA	GTCTGCCTTC	1680
TGATTTTTTCT	CTCTGAAAGT	CCCTGAAGGT	AGCACTACTG	GGCACAGAGT	GAAGTGTTC	1740
CACTTGATCT	TTCTGAACAA	GAGCAAAATA	CCCTCCATGC	CTTCTACGGA	AACGGAAGTT	1800
GCATGAAACA	ACCTCCGCTT	GGCTGTCTGG	TTTGTGGTAT	TACAGAGCTT	AATAAAAGAC	1860
TTAGATGTGA	AAAAAAAAAA	AAAAAAAAAA	AAAAAA			1896

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	1692 base pairs
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGTTATGTCT	GACTCACTGC	ACTGGAGTTT	GGCAAAAGCA	TCTCAGAAGT	GGTTGTGCTT	60
TTTTGAATGA	AATGATCAAT	GGAGTGCTCC	AGTTGTATGC	TGGCCTCTGG	ATACTAACTA	120
GACCTGCCTG	ACTCCAGGAA	CTAAGGCTCA	GTATCTGCAG	AAGCTTTTTG	CCCATCTCAT	180
TCCGGCTATG	GGGACAACAT	GTCTTCACCC	AGGAAGGTTA	GAGGAAAAAC	TGGAAGAGAT	240
AATGATGAAG	AGGAGGGTAA	TTCAGGTAAC	CTGAATCTCC	GCAACTCTTT	GCCTTCATCG	300
AGTCAGAAAA	TGACGCCTAC	GAAGCCGATT	TTTGGGAATA	AAATGAATTC	AGAGAATGTA	360
AAACCCTCCC	ATCACCTGTC	ATTCTCAGAT	AAGTATGAGC	TTGTTTACCC	AGAGCCTTTG	420
GAAAGTGACA	CTGATGAGAC	TGTGTGGGAT	GTCAGTGACC	GGTCTCTCAG	AAACAGGTGG	480
AACAGTATGG	ATTGAGAGAC	TGCAGGGCCG	TCAAAGACTG	TCTCCCCAGT	GCTTCTGGT	540
AGTAGTAGGC	TCTCAAAGGA	CACTGAAACA	TCTGTCTCTG	AAAAGGAGCT	AACTCAGTTG	600
GCTCAGATTC	GACCATTAA	ATTCAACAGT	TCTGCACGGT	CTGCTATGCG	GGATTGTTTG	660
AACACGCTTC	AGAAAAAAGA	AGAACTTGAT	ATCATCCGTG	AGTTTTTGGG	GTTAGAACAA	720
ATGACTCTGC	CTGATGACTT	CAATTCTGGG	AATACACTAC	AGAACAGAGA	TAAGAACAGA	780
TACCGAGATA	TTCTTCCATA	TGATTCAACA	CGTGTTCCTC	TTGGAAAAAA	CAAGGACTAC	840
ATCAACGCTA	GTTATATTAG	AATAGTAAAT	CATGAAGAAG	AGTATTTTTA	TATTGCCACT	900
CAAGGACCAT	TGCCAGAAAC	TATAGAAGAC	TTTTGGCAAA	TGGTCTTGGA	AAATAATTGT	960
AATGTTATTG	CTATGATAAC	CAGAGAGATA	GAATGTGGAG	TTATCAAGTG	TTACAGTTAC	1020

TGCCCCATTT	CTCTGAAGGA	GCCTTTGGAA	TTCGAACACT	TTAGTGTCTT	TCTGGAGACC	1080
TTTCATGTAA	CTCAATATTT	CACCGTTCGA	GTATTTTCAGA	TTGTGAAGAA	GTCCACAGGA	1140
AAGAGCCAAT	GTGTAAAACA	CTTGCAAGTC	ACCAAGTGGC	CAGACCATGG	CAC'TCCTGCC	1200
TCAGCAGATT	TTTTTCATAAA	ATATGTCCGT	TATGTGAGGA	AGAGCCACAT	TACAGGACCC	1260
CTCCTTGTTT	ACTGCAGTGC	TGGTGTAGGC	CGAACAGGGG	TGTTTCATATG	TGTGGATGTT	1320
GTGTTCTCTG	CCATCGAGAA	GAACTACTCT	TTTGACATTA	TGAACATAGT	GACCCAGATG	1380
AGAAAGCAGC	GCTGTGGCAT	GATTCAAACC	AAGGTTACCG	AGCAGCTTGG	AGCCTGAGCC	1440
GTGCTGAAGC	GTCTGCGGGC	CGTGCAGTCT	GCCTTCTGAT	TTTTCTCTCT	GAAAGTCCCT	1500
GAAGGTAGCA	CTACTGGGCA	CAGAGTGAAC	TGTTTCCACT	TGATCTTTCT	GAACAAGAGC	1560
AAAATACCCCT	CCATGCCTTC	TACGGAAACG	GAAGTTGCAT	GAAACAACCT	CCGCTTGGCT	1620
GTCTGGTTTG	TGGTATTACA	GAGCTTAATA	AAAGACTTAG	ATGTGAAAAA	AAAAAAAAAA	1680
AAAAAAAAAA	AA					1692

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	320 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAAAAATAATT	GTAATGTTAT	TGCTATGATA	ACCAGAGAGA	TAGAAGGTGG	AGTTATCAAG	60
TGTTGCAGTT	ACTGGCCCCGT	TTCTCTGAAG	GAGCCTTTGG	AATTCAAACA	CTTTCATGTC	120
CTTCTGGAGA	ACTTTCAGAT	AACTCAGTAT	TTTGTCATCC	GAATATTTCA	AATTGTGAAG	180
AAGTCCACAG	GAAAGAGTCA	CTCTGTAAAA	CAC'TTGCAGT	TCATCAAATG	GCCAGACCAT	240
GGCACTCCTG	CCTCAGTAGA	TTTTTTCATC	AAATATGTCC	GTTATGTGAG	GAAGAGCCAC	300
ATTACAGGAC	CCCTCCTTGT					320

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	426 amino acids
(B)	TYPE:	amino acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ser	Ser	Pro	Arg	Lys	Val	Arg	Gly	Lys	Thr	Gly	Arg	Asp	Asn	Asp
1				5					10					15	
Glu	Glu	Glu	Gly	Asn	Ser	Gly	Asn	Leu	Asn	Leu	Arg	Asn	Ser	Leu	Pro
			20					25					30		
Ser	Ser	Ser	Gln	Lys	Met	Thr	Pro	Thr	Lys	Pro	Ile	Phe	Gly	Asn	Lys
			35				40					45			
Met	Asn	Ser	Glu	Asn	Val	Lys	Pro	Ser	His	His	Leu	Ser	Phe	Ser	Asp
	50					55					60				
Lys	Tyr	Glu	Leu	Val	Tyr	Pro	Glu	Pro	Leu	Glu	Ser	Asp	Thr	Asp	Glu
	65				70				75					80	

Thr Val Trp Asp Val Ser Asp Arg Ser Leu Arg Asn Arg Trp Asn Ser
 85 90 95
 Met Asp Ser Glu Thr Ala Gly Pro Ser Lys Thr Val Ser Pro Val Leu
 100 105 110
 Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu Thr Ser Val Ser Glu
 115 120 125
 Lys Glu Leu Thr Gln Leu Ala Gln Ile Arg Pro Leu Ile Phe Asn Ser
 130 135 140
 Ser Ala Arg Ser Ala Met Arg Asp Cys Leu Asn Thr Leu Gln Lys Lys
 145 150 155 160
 Glu Glu Leu Asp Ile Ile Arg Glu Phe Leu Glu Leu Glu Gln Met Thr
 165 170 175
 Leu Pro Asp Asp Phe Asn Ser Gly Asn Thr Leu Gln Asn Arg Asp Lys
 180 185 190
 Asn Arg Tyr Arg Asp Ile Leu Pro Tyr Asp Ser Thr Arg Val Pro Leu
 195 200 205
 Gly Lys Asn Lys Asp Tyr Ile Asn Ala Ser Tyr Ile Arg Ile Val Asn
 210 215 220
 His Glu Glu Glu Tyr Phe Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu
 225 230 235 240
 Thr Ile Glu Asp Phe Trp Gln Met Val Leu Glu Asn Asn Cys Asn Val
 245 250 255
 Ile Ala Met Ile Thr Arg Glu Ile Glu Cys Gly Val Ile Lys Cys Tyr
 260 265 270
 Ser Tyr Trp Pro Ile Ser Leu Lys Glu Pro Leu Glu Phe Glu His Phe
 275 280 285
 Ser Val Phe Leu Glu Thr Phe His Val Thr Gln Tyr Phe Thr Val Arg
 290 295 300
 Val Phe Gln Ile Val Lys Lys Ser Thr Gly Lys Ser Gln Cys Val Lys
 305 310 315 320
 His Leu Gln Phe Thr Lys Trp Pro Asp His Gly Thr Pro Ala Ser Ala
 325 330 335
 Asp Phe Phe Ile Lys Tyr Val Arg Tyr Val Arg Lys Ser His Ile Thr
 340 345 350
 Gly Pro Leu Leu Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Val
 355 360 365
 Phe Ile Cys Val Asp Val Val Phe Ser Ala Ile Glu Lys Asn Tyr Ser
 370 375 380
 Phe Asp Ile Met Asn Ile Val Thr Gln Met Arg Lys Gln Arg Cys Gly
 385 390 395 400
 Met Ile Gln Thr Lys Glu Gln Tyr Gln Phe Cys Tyr Glu Ile Val Leu
 405 410 415

Glu Val Leu Gln Asn Leu Leu Ala Leu Tyr
 420 425

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Ser Pro Arg Lys Val Arg Gly Lys Thr Gly Arg Asp Asn Asp
 1 5 10 15
 Glu Glu Glu Gly Asn Ser Gly Asn Leu Asn Leu Arg Asn Ser Leu Pro
 20 25 30
 Ser Ser Ser Gln Lys Met Thr Pro Thr Lys Pro Val Gln Asn Lys Asn
 35 40 45
 Leu Met Lys Tyr Glu Glu His Leu Asp Ile Leu Met Val Phe Leu Leu
 50 55 60
 Ile Lys Thr Ile Trp Tyr Asn Val Phe Lys Leu Trp Lys Gly Lys Leu
 65 70 75 80
 Ile Phe Gly Asn Lys Met Asn Ser Glu Asn Val Lys Pro Ser His His
 85 90 95
 Leu Ser Phe Ser Asp Lys Tyr Glu Leu Val Tyr Pro Glu Pro Leu Glu
 100 105 110
 Ser Asp Thr Asp Glu Thr Val Trp Asp Val Ser Asp Arg Ser Leu Arg
 115 120 125
 Asn Arg Trp Asn Ser Met Asp Ser Glu Thr Ala Gly Pro Ser Lys Thr
 130 135 140
 Val Ser Pro Val Leu Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu
 145 150 155 160
 Thr Ser Val Ser Glu Lys Glu Leu Thr Gln Leu Ala Gln Ile Arg Pro
 165 170 175
 Leu Ile Phe Asn Ser Ser Ala Arg Ser Ala Met Arg Asp Cys Leu Asn
 180 185 190
 Thr Leu Gln Lys Lys Glu Glu Leu Asp Ile Ile Arg Glu Phe Leu Glu
 195 200 205
 Leu Glu Gln Met Thr Leu Pro Asp Asp Phe Asn Ser Gly Asn Thr Leu
 210 215 220
 Gln Asn Arg Asp Lys Asn Arg Tyr Arg Asp Ile Leu Pro Tyr Asp Ser
 225 230 235 240

(2) INFORMATION FOR SEQ ID NO:7:

(A) LENGTH: 405 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

SSSD/93680. v01

Ser Ser Ser Gln Lys Met Thr Pro Thr Lys Pro Ile Phe Gly Asn Lys
 35 40 45
 Met Asn Ser Glu Asn Val Lys Pro Ser His His Leu Ser Phe Ser Asp
 50 55 60
 Lys Tyr Glu Leu Val Tyr Pro Glu Pro Leu Glu Ser Asp Thr Asp Glu
 65 70 75 80
 Thr Val Trp Asp Val Ser Asp Arg Ser Leu Arg Asn Arg Trp Asn Ser
 85 90 95
 Met Asp Ser Glu Thr Ala Gly Pro Ser Lys Thr Val Ser Pro Val Leu
 100 105 110
 Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu Thr Ser Val Ser Glu
 115 120 125
 Lys Glu Leu Thr Gln Leu Ala Gln Ile Arg Pro Leu Ile Phe Asn Ser
 130 135 140
 Ser Ala Arg Ser Ala Met Arg Asp Cys Leu Asn Thr Leu Gln Lys Lys
 145 150 155 160
 Glu Glu Leu Asp Ile Ile Arg Glu Phe Leu Glu Leu Glu Gln Met Thr
 165 170 175
 Leu Pro Asp Asp Phe Asn Ser Gly Asn Thr Leu Gln Asn Arg Asp Lys
 180 185 190
 Asn Arg Tyr Arg Asp Ile Leu Pro Tyr Asp Ser Thr Arg Val Pro Leu
 195 200 205
 Gly Lys Asn Lys Asp Tyr Ile Asn Ala Ser Tyr Ile Arg Ile Val Asn
 210 215 220
 His Glu Glu Glu Tyr Phe Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu
 225 230 235 240
 Thr Ile Glu Asp Phe Trp Gln Met Val Leu Glu Asn Asn Cys Asn Val
 245 250 255
 Ile Ala Met Ile Thr Arg Glu Ile Glu Cys Gly Val Ile Lys Cys Tyr
 260 265 270
 Ser Tyr Trp Pro Ile Ser Leu Lys Glu Pro Leu Glu Phe Glu His Phe
 275 280 285
 Ser Val Phe Leu Glu Thr Phe His Val Thr Gln Tyr Phe Thr Val Arg
 290 295 300
 Val Phe Gln Ile Val Lys Lys Ser Thr Gly Lys Ser Gln Cys Val Lys
 305 310 315 320
 His Leu Gln Phe Thr Lys Trp Pro Asp His Gly Thr Pro Ala Ser Ala
 325 330 335
 Asp Phe Phe Ile Lys Tyr Val Arg Tyr Val Arg Lys Ser His Ile Thr
 340 345 350
 Gly Pro Leu Leu Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Val
 355 360 365

Phe Ile Cys Val Asp Val Val Phe Ser Ala Ile Glu Lys Asn Tyr Ser
 370 375 380
 Phe Asp Ile Met Asn Ile Val Thr Gln Met Arg Lys Gln Arg Cys Gly
 385 390 395 400
 Met Ile Gln Thr Lys
 405

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Phe Trp Gly Met Met Trp Glu Asn Asn Cys Asn Val Ile Ala Met
 1 5 10 15
 Ile Thr Arg Glu Ile Glu Gly Gly Val Ile Lys Cys Cys Ser Tyr Trp
 20 25 30
 Pro Val Ser Leu Lys Glu Pro Leu Glu Phe Lys His Phe His Val Leu
 35 40 45
 Leu Glu Asn Phe Gln Ile Thr Gln Tyr Phe Val Ile Arg Ile Phe Gln
 50 55 60
 Ile Val Lys Lys Ser Thr Gly Lys Ser His Ser Val Lys His Leu Gln
 65 70 75 80
 Phe Ile Lys Trp Pro Asp His Gly Thr Pro Ala Ser Val Asp Phe Phe
 85 90 95
 Ile Lys Tyr Val Arg Tyr Val Arg Lys Ser His Ile Thr Gly Pro Leu
 100 105 110
 Leu Val His Cys Thr Ala Gly Val Gly Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "Y" stands for C or T.

The letter "V" stands for A, C or G.

The letter "R" stands for A or G.

The letter "N" stands for A, C, G or T.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAYTTYTGGV RNATGRTNTG GGA

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "S" stands for C or G.
The letter "Y" stands for C or T.
The letter "N" stands for A, C, G or T.
The letter "W" stands for A or T.
The letter "R" stands for A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGCCSAYNC CNGCNSWRCA RTG

23

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in positions 4 and 6 stand for an unspecified amino acid.
"Xaa" in position 8 stands for either Glu or Asp.

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asp Phe Trp Xaa Met Xaa Trp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (D) OTHER INFORMATION: "Xaa" in positions 3 and 6 stand for an unspecified amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

His Cys Xaa Ala Gly Xaa Gly
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACCGTTCGA GTATTCAGA TTGTGAAGAA GTCC

34

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGACTTCTTC ACAATCTGAA ATACTCGAAC GGTG

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- ```
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCGTTATGTG AGGAAGAGCC ACATTACAGG ACC

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTCCTGTAA TGTGGCTCTT CCTCACATAA CGG

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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CACCGTTCGA GTATTCAGA TTGTGAAGAA GTCC

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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGTCCTGTAA TGTGGCTCTT CCTCACATAA CGG

33

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

His Cys Ser Ala Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ser Ser Pro Arg Lys Val Arg Gly Lys Thr Gly Arg Asp Asn Asp  
1 5 10 15

Glu Glu Glu Gly Asn Ser Gly Asn Leu Asn Leu Arg Asn  
20 25

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ser Pro Val Leu Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu Thr  
 1 5 10 15  
 Ser Val Ser Glu Lys Glu Leu Thr Gln Leu Ala Gln Ile  
 20 25

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Trp Asp Val Ser Asp Arg Ser Leu Arg Asn Arg Trp Asn Ser Met Asp  
 1 5 10 15  
 Ser Glu Thr Ala Gly Pro Ser Lys Thr Val Ser Pro Val  
 20 25

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